Figure S1. Distribution of the observed and expected numbers of changes between geographical states in the U.S. and Canada. Each taxon was categorized as a U.S. state or Canadian province (see Table S1) according to where its sequence was isolated. The numbers of observed state changes were counted between the taxon location state and the ancestral location states, as inferred using a parsimony procedure on 200 maximum likelihood bootstrap trees. The expected numbers were counted from 500 randomizations of taxon states for each of the 200 bootstrap trees (i.e. 100,000 randomizations in total).

PB2

NS (allele A)

NS (allele B)

HA (H3)

HA (H4)

NA (N6)

NA (N8)

PB1

PA (lineage B)

PA (lineage A)

NP

MP

Observed value (S)   Expected value (S_P)

Number of all state changes between different
geographical states in U.S. and Canada